

## SEQUENCE LISTING

<110> Mockel, Bettina  
Pfefferle, Walter  
Marx, Achim

<120> New Nucleotide Sequences Coding for the Genes sucC and sucD

<130> 21123/278466

<140> 09/838,564

<141> 2001-04-20

<160> 5

<170> PatentIn version 3.0

<210> 1

<211> 2410

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (142)..(1347)

<223> sucC sequence

<220>

<221> CDS

<222> (1372)..(2253)

<223> sucD sequence

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gatcatattg gtgagttgaa acacttactt ttacgggaag actttgttaa agacgcagaa 120

ggctotaagc atgggcccga a atg gaa ttg gca gtg gat ctt ttt gaa tac 171  
Met Glu Leu Ala Val Asp Leu Phe Glu Tyr  
1 5 10

caa gca cgg gac ctc ttt gaa acc cat ggt gtg cca gtg ttg aag gga 219  
Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly  
15 20 25

att gtg gca tca aca cca gag gcg gcg agg aaa gcg gct gag gaa atc Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile 30 35 40	267
ggc gga ctg acc gtc gtc aag gct cag gtc aag gtg ggc gga cgt ggc Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly 45 50 55	315
aag gcg ggt ggc gtc cgt gtg gca ccg acg tcg gct cag gct ttt gat Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp 60 65 70	363
gct gcg gat gcg att ctc ggc atg gat atc aaa gga cac act gtt aat Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn 75 80 85 90	411
cag gtg atg gtg gcg cag ggc gct gac att gct gag gaa tac tat ttc Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe 95 100 105	459
tcc att ttg ttg gat cgc gcg aat cgt tcg tat ctg gct atg tgc tct Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser 110 115 120	507
gtt gaa ggt ggc atg gag atc gag atc ctg gcg aag gaa aag cct gaa Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu 125 130 135	555
gct ttg gca aag gtg gaa gtg gat ccc ctc act ggt att gat gag gac Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp 140 145 150	603
aaa gcg cgg gag att gtc act gct gct ggc ttt gaa act gag gtg gca Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala 155 160 165 170	651
gag aaa gtc att ccg gtg ctg atc aag atc tgg cag gtg tat tac gaa Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu 175 180 185	699
gag gaa gca aca ctc gtt gag gtg aac ccg ttg gtg ctc acg gat gac Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp 190 195 200	747
ggc gat gtg att gcg ctt gat ggc aag atc acg ctg gat gat aac gct Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala 205 210 215	795
gat ttc cgc cat gat aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc Asp Phe Arg His Asp Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly 220 225 230	843
ttg gac att ttg gaa ctg aag gcc aag aag aat gat ctg aac tac gtg Leu Asp Ile Leu Glu Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val 235 240 245 250	891
aaa ctt gat ggc tct gtg ggc atc att ggc aat ggt gca ggt ttg gtg Lys Leu Asp Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val 255 260 265	939

atg tcc acg ttg gat atc gtg gct gca gct ggt gaa cgc cat ggt ggg Met Ser Thr Leu Asp Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly	987
270 275 280	
cag cgc ccc gcg aac ttc cta gac att ggt ggc gga gca tca gct gaa Gln Arg Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu	1035
285 290 295	
tcg atg gct gct ggt ctc gat gtg atc ctt ggg gat agc cag gta cgc Ser Met Ala Ala Gly Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg	1083
300 305 310	
agt gtg ttt gtg aat gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val	1131
315 320 325 330	
gca aag gga atc gtt gga gct ttg gat gtg ctc ggc gat caa gca acg Ala Lys Gly Ile Val Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr	1179
335 340 345	
aag cct ctt gtg gtg cgc ctt gat ggc aac aac gtg gtg gaa ggc aga Lys Pro Leu Val Val Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg	1227
350 355 360	
cga atc ctc gcg gaa tat aac cac cct ttg gtc acc gtt gtg gag ggt Arg Ile Leu Ala Glu Tyr Asn His Pro Leu Val Thr Val Val Glu Gly	1275
365 370 375	
atg gat gca gcg gct gat cac gct gcc cat ttg gcc aat ctt gcc cag Met Asp Ala Ala Ala Asp His Ala Ala His Leu Ala Asn Leu Ala Gln	1323
380 385 390	
cac ggc cag ttc gca acc gct aat tagttaagga gcacctgttt aatc atg His Gly Gln Phe Ala Thr Ala Asn Met	1374
395 400	
tct att ttt ctc aat tca gat tcc cgc atc atc att cag ggc att acc Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile Thr	1422
405 410 415	
ggt tcg gaa ggt tca gag cat gcg cgt cga att tta gcc tct ggt gcg Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly Ala	1470
420 425 430 435	
aag ctc gtg ggt ggc acc aac ccc cgc aaa gct ggg caa acc att ttg Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile Leu	1518
440 445 450	
atc aat gac act gag ttg cct gta ttt ggc act gtt aag gaa gca atg Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala Met	1566
455 460 465	
gag gaa acg ggt gcg gat gtc acc gta att ttc ggt cct cca gcc ttt Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala Phe	1614
470 475 480	
gcc aaa gct gcg atc att gaa gct atc gac gct cac atc cca ctg tgc Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu Cys	1662
485 490 495	

gtg att att act gag ggc atc cca gtg cgt gac gct tct gag gcg tgg Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp 500 505 510 515	1710
gct tat gcc aag aag gtg gga cac acc cgc atc att ggc cct aac tgc Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn Cys 520 525 530	1758
cca ggc att att act ccc ggc gaa tct ctt gcg gga att acg ccg gca Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala 535 540 545	1806
aac att gca ggt tcc ggc ccg atc ggg ttg atc tca aag tcg gga aca Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr 550 555 560	1854
ctg act tat cag atg atg tac gaa ctt tca gat att ggc att tct acg Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr 565 570 575	1902
gcg att ggt att ggc ggt gac cca atc atc ggt aca acc cat atc gac Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp 580 585 590 595	1950
gct ctg gag gcc ttt gaa gct gat cct gag acc aag gca atc gtc atg Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met 600 605 610	1998
atc ggt gag atc ggt gga gat gca gag gaa cgc gct gct gac ttc att Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile 615 620 625	2046
tct aag cac gtg aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr 630 635 640	2094
gcc cct gaa gga aag acc atg ggg cat gct ggc gcc atc gtg aca ggt Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly 645 650 655	2142
tca gaa ggc act gcg cga gca aag aag cat gca ttg gag gcc gtg ggt Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly 660 665 670 675	2190
gtt cgc gtg gga aca act ccg agt gaa acc gcg aag ctt atg cgt gag Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu 680 685 690	2238
gta gtt gca gct ttg taactaacag gccacagatc ttagctttga ccagcggatt Val Val Ala Ala Leu 695	2293
tgtygctaat cgcgcggctct gtgtagagta ttcattctgtg cgcaggacag tgtgacaaac	2353
actgaatagt gcatggcttt aaggccctgt ggcgcagttg gttagcgcgc cgccctg	2410

&lt;210&gt; 2

&lt;211&gt; 402

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

<400> 2

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Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr Pro  
20 25 30

Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val Val  
35 40 45

Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val Arg  
50 55 60

Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile Leu  
65 70 75 80

Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala Gln  
85 90 95

Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp Arg  
100 105 110

Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met Glu  
115 120 125

Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val Glu  
130 135 140

Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile Val  
145 150 155 160

Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro Val  
165 170 175

Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu Val  
180 185 190

Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala Leu  
195 200 205

Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp Asn  
210 215 220

Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu Leu  
225 230 235 240

Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser Val  
245 250 255

Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp Ile  
260 265 270

Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn Phe  
275 280 285

Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly Leu  
290 295 300

Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn Val  
305 310 315 320

Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val Gly  
325 330 335

Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val Arg  
340 345 350

Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu Tyr  
355 360 365

Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala Asp  
370 375 380

His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala Thr  
385 390 395 400

Ala Asn

<210> 3

<211> 294

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 3

Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile  
1 5 10 15

Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly  
20 25 30

Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile  
35 40 45

Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala  
50 55 60

Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala  
65 70 75 80

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu  
85 90 95

Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala  
100 105 110

Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn  
115 120 125

Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro  
130 135 140

Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly  
145 150 155 160

Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser  
165 170 175

Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile  
180 185 190

Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val  
195 200 205

Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe  
210 215 220

Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe  
225 230 235 240

Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr  
245 250 255

Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val  
260 265 270

Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg  
 275 280 285

Glu Val Val Ala Ala Leu  
 290

<210> 4

<211> 1206

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(1206)

<223> sucC coding sequence

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gaa acc cat ggt gtg tca gtg ttg aag gga att gtg gca tca aca cca	96
Glu Thr His Gly Val Ser Val Leu Lys Gly Ile Val Ala Ser Thr Pro	
20 25 30	
gag gcg gcg agg aaa gcg gct gag gaa atc ggc gaa ctg acc gtc gtc	144
Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Glu Leu Thr Val Val	
35 40 45	
aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc cgt	192
Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val Arg	
50 55 60	
gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att ctc	240
Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile Leu	
65 70 75 80	
ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg cag	288
Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala Gln	
85 90 95	
ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat cgc	336
Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp Arg	
100 105 110	
gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg gag	384
Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met Glu	
115 120 125	
atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg gaa	432
Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val Glu	
130 135 140	



gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att gtc Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile Val 145 150 155 160	480
act gct gct ggc ttt gaa act gag gtg aca gag aaa gtc att ccg gtg Thr Ala Ala Gly Phe Glu Thr Glu Val Thr Glu Lys Val Ile Pro Val 165 170 175	528
ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc gtt Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu Val 180 185 190	576
gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg ctt Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala Leu 195 200 205	624
gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat aac Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp Asn 210 215 220	672
cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa ctg Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu Leu 225 230 235 240	720
aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct gtg Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser Val 245 250 255	768
ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat atc Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp Ile 260 265 270	816
gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac ttc Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn Phe 275 280 285	864
cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt ctc Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly Leu 290 295 300	912
gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat gtg Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn Val 305 310 315 320	960
ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt gga Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val Gly 325 330 335	1008
gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg cgc Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val Arg 340 345 350	1056
ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa tat Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu Tyr 355 360 365	1104
aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct gat Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala Asp 370 375 380	1152

cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca acc 1200  
 His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala Thr  
 385 390 395 400

gct aat 1206  
 Ala Asn

<210> 5

<211> 402

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 5

Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu Phe  
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Glu Thr His Gly Val Ser Val Leu Lys Gly Ile Val Ala Ser Thr Pro  
 20 25 30

Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Glu Leu Thr Val Val  
 35 40 45

Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val Arg  
 50 55 60

Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile Leu  
 65 70 75 80

Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala Gln  
 85 90 95

Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp Arg  
 100 105 110

Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met Glu  
 115 120 125

Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val Glu  
 130 135 140

Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile Val  
 145 150 155 160

Thr Ala Ala Gly Phe Glu Thr Glu Val Thr Glu Lys Val Ile Pro Val  
 165 170 175

Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu Val  
 180 185 190

Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala Leu  
 195 200 205

Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp Asn  
 210 215 220

Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu Leu  
 225 230 235 240

Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser Val  
 245 250 255

Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp Ile  
 260 265 270

Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn Phe  
 275 280 285

Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly Leu  
 290 295 300

Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn Val  
 305 310 315 320

Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val Gly  
 325 330 335

Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val Arg  
 340 345 350

Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu Tyr  
 355 360 365

Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala Asp  
 370 375 380

His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala Thr  
 385 390 395 400

Ala Asn